UNITED STATES DISTRICT COURT
SOUTHERN DISTRICT OF NEW YORK
UNITED STATES OF AMERICA,

v. 15 Cr. 153 (VSB)

DEAN JONES,

Defendant.
_____

DEFENDANT DEAN JONES MEMORANDUM OF LAW IN SUPPORT OF HIS MOTION TO EXCLUDE EVIDENCE PRODUCED BY THE FORENSIC STASTICAL TOOL AND REQUEST FOR A *Daubert* HEARING

Donald duBoulay, esq
Counsel for Dean Jones
305 Broadway, Suite 602
New York, New York 10007
(212) 966-3970

INTRODUCTION

Defendant Dean Jones respectfully submits this memorandum of law with accompanying exhibits in support of his motion, pursuant to Fed.R.Evid 104 (a),401,402,403 and 702, to exclude any evidence at trial produced by the Forensic Statistical Tool test results, and to request a *Daubert* hearing.

Factual Background

1. Dean Jones was arrested on June 14, 2013 by the New York City Police. He was arraigned in Criminal Court on June 16, 2013, and charged with attempted murder in the second degree, and other related charges, for conduct that allegedly occurred on December 21, 2012. Mr. Jones was subsequently removed to the Federal Court for prosecution for violating the terms of his supervised release on December 29, 2014. He was thereafter indicted for the instant offenses on March 13, 2015 A trial of this matter is scheduled for January 11, 2015

2. On December 21, 2012, New York City Police Department ("NYPD") law enforcement personnel recovered a hat and glove from the vicinity of 1697 and 1701 Nelson Avenue, in the Bronx. The hat was scraped for DNA and the glove was swabbed for DNA. The scrapings from the hat and the swabs from the glove were subsequently analyzed by a criminalist at the Office of Chief Medical Examiner ("OCME"), Department of Forensic Biology.

3. Meanwhile, a court ordered Mr. Jones to submit to a buccal swab—which he did—so that his DNA profile could be developed by the OCME as well.

The Laboratory Reports Issued by the OCME

4. The OCME produced two Laboratory Reports summarizing its conclusions regarding the DNA testing conducted in this case. The first, dated December 11, 2013, (attached as Exhibit A), indicates that DNA testing performed on the hat scrapings revealed a "mixture of

DNA from at least two people, including at least one major male contributor, Male Donor A," but the "DNA profile(s) of the minor contributor(s) to th[e] mixture could not be determined. . . ." Exhibit A at 2. The testing performed on the glove swabs, meanwhile, revealed a "mixture of DNA from at least three people," but the "profiles of the individual contributors to the mixture could not be determined." *Id.*

5. The second report, dated June 10, 2014, (attached as Exhibit B), summarizes conclusions drawn by the criminalist after she had developed Mr. Jones's DNA profile from the buccal swab he submitted. The report draws two main conclusions. First, the criminalist concluded that Mr. Jones's DNA profile was "consistent with those of Male Donor A," so based on the random match probability for unrelated individuals, "Dean Jones is the source of the DNA found" on the hat scrapings. Exhibit B at 1. Second—and the conclusion relevant to this Motion—the criminalist decided that because Mr. Jones "cannot be ruled out as a contributor" to the DNA found on the glove swabs, the FST software would be used to calculate a likelihood ratio. *Id.* at 2. The results from the FST software, expressed both quantitatively and qualitatively, were as follows:

> The DNA mixture found on the glove swabs is approximately 1340 times more probable if the sample originated from [] Dean Jones and two unknown, unrelated persons than if it originated from three unknown, unrelated person.
>
> Therefore, there is very strong support that Dean Jones and two unknown, unrelated persons contributed to this mixture, rather than three unknown, unrelated persons.

Id. at 2.

6. According to the Report, "Cannot be excluded as a contributor to the mixture" means the following:

> For the locations where comparisons could be made, most of the DNA alleles seen in an individual's DNA profile were also seen in the mixture. The allele(s) that were absent could be explained by any of several factors. Therefore, this person cannot be ruled out as a contributor.

Exhibit B at 5. The OCME also defines other terms it uses to explain the variety of DNA testing conclusions available, *see id.*, but the OCME personnel determined that none of the other conclusions were applicable to the test results in this case. Other such conclusions include:

> Is a major or minor contributor to the mixture: The DNA profile of an individual matches a major or minor evidentiary DNA profile determined from a mixture, and the DNA population frequency of the determined major or the minor DNA profile meets the threshold of 1 in greater than 6.80 trillion individuals, assuming that source is not an identical twin.
>
> Could be a major or minor contributor to the mixture: The DNA profile of an individual is consistent with a major or minor evidentiary DNA profile determined from a mixture, and the DNA population frequency of the determined major or the minor DNA profile does not meet the threshold of 1 in greater than 6.80 trillion unrelated people.
>
> Could be a contributor to the mixture: For mixtures where individual profiles were not determined, all of the DNA alleles seen in an individual's DNA profile were also seen in the mixture for the locations where comparisons could be made.
>
> Excluded as a contributor to the mixture: For the locations where comparisons could be made, one or more of the DNA alleles seen in an individual's DNA profile were not seen in the mixture and this absence cannot be explained. Therefore, this person can be ruled out as a contributor.
>
> No conclusions can be drawn: The results do not support a positive association or an exclusion. Therefore, it cannot be determined whether a person can or cannot be excluded to the mixture.

Id. at 5. The OCME Report provides no further definition of these phrases for reporting conclusions, nor does it provide information about the methodology used to develop these phrases and definitions.

7. Within the second report issued by the OCME, therefore, are two strikingly different conclusions expressing the association between Mr. Jones's DNA profile and the mixture of DNA found on the glove swabs, without further explanation. First, that he merely *could not be ruled out as a possible contributor*; second, that *it is 1340 times more probable that the mixture originated from Mr. Jones and two other people than not*, providing very strong support for the notion that he did contribute to the mixture.

Background to Forensic DNA Analysis

8. Understanding FST requires an understanding of general principles relevant to DNA testing. DNA is a molecule containing genetic material that codes for the unique physical characteristics of human beings. An individual inherits half of his DNA from his mother and half from his father. Each person's DNA is unique, with the exception of identical twins.

9. DNA is comprised of four chemicals called nucleotides, or bases: adenine ("A"), cytosine ("C"), guanine ("G"), and thymine ("T"). These bases pair together in the following way: A with T; C with G. These pairs repeat in varying lengths and form the rungs on the double helix that constitutes the DNA molecule. The double helix is wound very tightly into a chromosome.

10. A gene is a unit along that double helix that comprises a given sequence of these base pairs. Different genes are located in different places, or loci, along a chromosome. An allele is one of several alternative forms of a gene. In other words, an allele is a variation in the number of times the base pairs of DNA repeat at a particular locus. Modern forensic analysis

focuses on Short Tandem Repeats (STRs), which refers to the particular way the nucleotides repeat at each locus. STRs exhibit high variability, meaning they vary from one person to another. By measuring the number of repeats at a given locus, an analyst can use STRs to distinguish one individual from another. Currently, in developing a DNA profile, the OCME examines fifteen loci, plus the gender-determining locus, named "Amelogenin." Numbers are used to represent which alleles are present at each locus. Each person has two alleles at each locus (one from each parent).

11. Current forensic DNA analysis is essentially a six-step process. First, DNA is extracted from the evidence, e.g. the swabs or scrapings taken from the physical evidence (a hat and glove in this case). In the second step, quantitation, the analyst measures the amount of DNA present in the sample being tested. The third step, amplification, involves polymerase chain reaction (PCR), a process of heating and cooling that makes millions of reproductions of DNA so that the DNA sample becomes more robust, and more easily analyzed.

12. In the fourth step, after the DNA is amplified, a process known as electrophoresis separates the STR fragments by size. The electrophoresis results appear as a series of peaks on a graph, known as an electropherogram. Once the electropherogram is generated, the analyst reviews it and draws conclusions about the DNA sample, with a view toward developing a DNA profile, thus constituting the fifth step. In the sixth and final step, the analyst can compare a forensic DNA profile with a known DNA profile, and draw additional conclusions.

13. Sometimes, when a mixture of DNA from two or more people is involved, an analyst cannot determine the DNA profile of any of the contributors to the forensic mixture. In such a case, the analyst can merely determine the least number of possible contributors to the

mixture and, until recently, draw a general conclusion as to whether a given suspect could be included or excluded as a possible contributor to the mixture.

14. It is at this stage where FST is utilized. Upon information and belief, the OCME's forensic DNA analysis in this case involves a relatively new DNA testing method. According to Dr. Caragine co-creator of the FST software, FST was developed by the OCME and officially put into use as a tool for calculating possible likelihood ratios on forensic samples containing mixtures on July 1, 2011. Dr. Caragine has also stated that the FST software program was tested extensively within the OCME, but acknowledged that it was developed in-house and is proprietary software and has neither been tested nor validated by any other lab or scientific body. FST calculates a likelihood ratio statistic in an attempt to quantify the likelihood that, given the DNA mixture at issue, the mixture originated from the DNA of a suspect and other contributors. This software purports to produce a result that can replace the previously-used terms such as "could be a contributor" or "cannot be excluded as a contributor," for example.

15. According to Dr. Caragine, to get to the resultant likelihood ratio, the software program assumes that a phenomenon known as "allelic drop-out" occurs with some predictable frequency in forensic samples containing mixtures of DNA. "Drop-out" occurs when an allele is not seeing in a given DNA profile, though the analyst would have expected to see the allele. This assumption is based upon studies of allelic drop-out rates done within the OCME. The software is not programmed to read, and therefore does not consider, the "raw data" or the relevant electropherograms produced during analysis of the forensic mixtures in a given case.

16. The data upon which the FST program relies, rather, is based on the analyst's interpretation of the electropherograms. Accordingly, after the analyst reviews the electropherograms and makes a determination regarding which alleles are present at each locus

in a forensic mixture, the analyst inputs this information, along with a known suspect profile, into the FST software. The analyst then sets the parameters for running the program including, for example, whether the calculation should be based on a mixture of at least two or at least three people (the FST software cannot be used if the mixture is determined by the analyst to come from at least four contributors). The software then outputs a "Forensic Statistic Comparison Report," summarizing the data that was input and indicating the resultant likelihood ratio. Four different likelihood ratios are output, each associated with a different ethnic group—Asian, Black, Caucasian, Hispanic. According to Dr. Caragine, the lowest likelihood ratio of the four produced is used in creating the final laboratory report and reporting the results.

17. As stated above, before July 1, 2011, the OCME could only assign a statistical probability known as the "Random Match Probability" to single source samples and to those samples containing DNA mixtures from more than one person from which a major or minor contributor to the sample could be deconvoluted. In the case of a mixture with no deducible profiles, meanwhile, the OCME would conclude that a defendant "could be a contributor," "could not be excluded," or that "no conclusion could be drawn," to take a few examples, regarding whether the defendant contributed to the sample.

18. When interpreting forensic mixtures, there are many controversial assumptions that must be invoked before performing a likelihood ratio in the first place, and likelihood ratios are only as good as the assumptions used to calculate them. In other words, if the calculation is based on an erroneous assumption (for example, that the mixture contains the profiles of two, not three people, or vice-versa, or three, not four people), the calculation is of no probative value. Furthermore, mixtures can be extremely complex and subjective to deconvolute. *See generally* Itiel E. Dror and Greg Hampikian, *Subjectivity and bias in forensic DNA mixture interpretation*,

Science and Justice 51, 204-208 (2011) (attached as Exhibit C). The complications of mixture interpretation include estimates about, *inter alia*: (1) the number of potential contributors to the mixture; (2) the degree of relatedness of the contributors, if any; (3) whether the contributors have no, few, or many shared alleles, and if any, which alleles are in fact shared; (4) whether the amount of DNA contributed by each contributor is sufficient to allow for a given degree of source attribution; (5) whether an appropriate amount and cross-section of DNA was amplified such that the DNA of all contributors is detected at levels above the laboratory's analytical threshold; (6) whether there was any degradation, inhibition, or stochastic effects that would interfere with interpretation and affect peak heights and the apparent DNA ratios; and (7) whether potential stutter peaks and any other artifacts are properly identified and edited out or erroneously identified and edited out. These complexities inherent to mixture interpretation are compounded by the assumptions and risk of analyst bias associated with mixture analysis, *see id*.

19. Dr. Caragine has acknowledged, for example, that the assumption that allelic drop-out, i.e. the non-detection of an allele believed, nevertheless, to be present in the DNA sample, occurs has been built into the OCME's FST software and forms the basis for its statistical calculations. *See generally* Adele A. Mitchell et al., *Validation of a DNA mixture statistics tool incorporating allelic drop-out and drop-in*, Forensics Science International: Genetics 6, 749-761 (2012) (attached as Exhibit D). Drop-out rate is just one of many assumptions built into the FST software and upon whose reliability the software depends in order to potentially yield a reliable result.

20. Indeed, the calculation of a likelihood ratio using the FST software is not within the best scientific practices of STR DNA interpretation. The Scientific Working Group on DNA Analysis Methods ("SWGDAM"), a "group of approximately 50 scientists representing federal,

state and local forensic DNA laboratories in the United States and Canada," has issued "Interpretation Guidelines for Autosomal STR Typing by Forensic DNA Testing Laboratories," to promote best scientific practices, including mixture interpretation.[1] With respect to statistical analyses generally:

> Whenever the statistical analysis at a locus is meant to represent all possible contributors to a mixture, if there is a reasonable possibility that locus dropout could have led to the loss of an entire genotype, then a statistical calculation should *not* be performed for that locus. Similarly, the product rule should not be applied when the resultant set of combined profiles would not include all individuals who would not be excluded as possible contributors to the mixture.

Guideline 5.1, at 15 (emphasis added). With respect to likelihood ratio ("LR") calculations in particular:

> The calculation of the LR in a mixture is dependent upon the evidence profile, the comparison reference profile(s), and the individual hypotheses. Given the myriad possible combinations, any list would be necessarily incomplete.

Guideline 5.4.2, at 19. Because likelihood ratio calculations performed by the FST software assume, *inter alia*, the occurrence of allelic drop-out, these calculations contravene the SWGDAM best practices guidelines.

21. Further, the OCME's FST software was developed by the OCME itself, and has not been adequately subjected either to validation or peer review by the relevant scientific community. Thus, it has not gained general acceptance within the scientific community. While the OCME maintains that they have subjected FST to extensive in-house testing, that they make conservative likelihood estimations, and that their accurately software accounts for the necessary variables, these claims have very little merit without rigorous scrutiny by anyone else outside the OCME, let alone the relevant scientific community. Indeed, a 1992 report authored by the

[1] *Available at* http://swgdam.org/Interpretation_Guidelines_January_2010.pdf.

Committee on DNA Technology in Forensic Science of the National Research Council, an arm of the National Academy of Sciences, contained the following recommendation to ensure high standards within the forensic DNA testing community:

> Quality-assurance programs in individual laboratories alone are insufficient to assure high standards. External mechanisms are needed, to ensure adherence to the practices of quality assurance.

National Academy of Sciences, *DNA Technology in Forensic Science*, at 109 (1992).

The OCME's Use of FST in Forensic DNA Analysis

22. The OCME is the only laboratory in the United States that uses the FST software for the purpose of analyzing DNA evidence and generating a result to use against a criminal defendant in a criminal case in court.

23. Additional information has been revealed more recently that bears upon the admissibility of FST results under *Daubert* as well. Most notably, in December 2013, the Office of the Inspector General ("OIG") for the State of New York conducted an "Investigation into the New York City Office of Chief Medical Examiner: Department of Forensic Biology," which is attached as Exhibit E. In its report, the OIG found that Dr. Theresa Caragine one of the co-creators of the FST software twice "ignored laboratory protocol regarding resolution of scientific disputes by rewriting a final report and reassigning cases when she disagreed with the findings rather than bringing them to the DNA technical leader for arbitration." Exhibit E at 43. After being confronted with these cases, Dr. Caragine, co-creator of the FST software, resigned on April 19, 2013. *Id.* at 44.

24. Subsequent to Dr. Caragine resigning, Dr. Adele Mitchell, the other co-creator of the FST software, also left the OCME's Department of Forensic Biology. Thus, neither co-creator of the FST software is employed any longer with the OCME.

ARGUMENT

The prosecution in this case intends to offer expert testimony related to the OCME's FST software and conclusions drawn from the use of that software. Specifically, the prosecution will offer one or more employees of the OCME to testify that using the OCME's FST software, a likelihood ratio was calculated indicating that, among other things:

> The DNA mixture found on the glove swabs is approximately 1340 times more probable if the sample originated from [] Dean Jones and two unknown, unrelated persons than if it originated from three unknown, unrelated persons.
>
> Therefore, there is very strong support that Dean Jones and two unknown, unrelated persons contributed to this mixture, rather than three unknown, unrelated persons.

Exhibit B.

While forensic DNA testing has long been admissible in Federal Courts *U.S.v. Jakobetz* 955 F.2d 786 (2nd Cir. 1992), FST software relating to forensic DNA testing is a recently developed, novel technique that is not generally accepted as reliable in the forensic DNA community. *People v. Andrew Peaks & Jaquan Collins*, Indictment Nos. 7689-10 & 8077-10 (Sup. Ct. Kings Co. November 7, 2014). To the extent that FST has undergone some validation and/or peer review, the technique is still in its early stages and admitting expert testimony about it in a criminal case, where a defendant's liberty is at stake, would be premature and would short-circuit the debate necessary to determine the accuracy of the technique. Indeed, given the exclusively internal validation that OCME conducted, very few experts within the DNA forensic community are even knowledgeable about the workings of the FST software. Thus, this Court should preclude the prosecution from introducing expert testimony regarding the use of the OCME's FST software. Alternatively, *a Daubert* hearing should be conducted.

The *Daubert* Standard

Federal Rule of Evidence 702 allows for the admissibility of expert testimony so long as "(1) the testimony is based upon sufficient facts or data, (2) the testimony is the product of reliable principles and methods, and (3) the expert has applied the principles and methods reliably to the facts of the case." Fed. R. Evid. 702. The district court has a "gatekeeping" function under Rule 702, and is charged with "the task of ensuring that an expert's testimony both rests on reliable foundation and is relevant to the task at hand." *Daubert v. Merrell Dow Pharmaceuticals,Inc*., 509 U.S. 579,597 (1993). In assessing the admissibility of expert evidence, a district court should be mindful of other applicable rules, including Rule 403, which permits the exclusion of evidence if its "probative value is substantively outweighed by a danger of…unfair prejudice, confusing the issues, or misleading the jury…"*Id*. at 595;Fed.R.Evid. 403.

As part of its "gatekeeping" function, the district court must make a "preliminary assessment of whether the reasoning or methodology underlying the testimony is scientifically valid and of whether that reasoning or methodology properly can be applied to the facts in issue." *Daubert*, 509 U.S. at 592. The Court has "considerable leeway" in "deciding how to test an expert's reliability, and to decide whether or when special briefing or other proceedings are needed to investigate reliability." *Kumho Tire Co. v. Carmichael*, 526 U.S. 137,152 (1999).

Thus in a *Daubert* inquiry, the Court must preliminarily ensure that the proposed scientific testimony "is not only relevant, but reliable". Id, at 589; see *Ruggiero v. Warner – Lambert Co*., 424 F.3d 249, 253 (2d Cir. 2005). In *Daubert*, the Supreme Court identified a number of factors bearing on reliability that district courts may consider, such as: (1) whether a theory or technique "can be (and has been) tested"; (2) whether the theory or technique "has been subjected to peer review and publication" ; (3) a technique's "known or potential rate of error,"

and the existence and maintenance of standards controlling the technique's operation," and (4) whether a particular technique or theory has gained "general acceptance" in the "relevant scientific community." *Daubert*, 509 U.S. at 593-594. These factors are not an exhaustive "definitive checklist or test", *Daubert* at 594, and "the trial judge must have considerable leeway in deciding in a particular case how to go about determining whether particular expert testimony is reliable." *Kumho Tire Co*, 526 U.S. at 152.

Other factors that courts may consider in a Daubert inquiry include: (1) whether the expert has unjustifiably extrapolated from an accepted premise to an unfounded conclusion, see *General Electric v. Joiner*, 522 U.S. 136, 146 (1997) (noting that a trial court "may conclude that there is simply too great an analytical gap between the data and the opinion proffered"); (2) whether the field of expertise claimed by the expert is known to reach reliable results for the type of opinion the expert would give, see *Kumho* Tire Co., 526 U.S. at 151-152; and (3) whether the expert has adequately accounted for obvious alternative explanations. See, *Claar v. Burlington* ., *N.R.R.*, 29 F.3d 499 (9th Cir 1994). Thus 'when an expert opinion is based on a methodology, or studies that are simply inadequate to support the conclusions reached, *Daubert* and Rule 702 mandate the exclusion of that unreliable opinion testimony." *Amorgianos v. Amtrak*, 303 F.3d 256,266 (2d Cir. 2002).

In the context of a *Daubert* inquiry the "district court must focus on the principles and methodology employed by the expert," however, the conclusions drawn by the expert are also relevant. *Amorgianos*, 303 F.3d at 266. The Supreme court has stated,

> Conclusions and methodology are not entirely distinct from one another…Nothing in either *Daubert* or the Federal Rules of Evidence requires a district court to admit opinion evidence that is connected to existing data only by the ipse dixit of the expert. A court may conclude that there is simply too great an analytical gap between the data and the opinion evidence.

General Electric v. Joiner, 522 U.S. 136,146 (1997)

"To warrant admissibility, however, it is critical that an expert's analysis be reliable at every step" *Amorgianos*, 303 F.3d at 267. Further, an expert's analysis conclusion's must be "supported by good grounds for each step in the analysis" and 'any step that renders the analysis unreliable under the *Daubert* factors renders the expert's testimony inadmissible." *Amorgianos*, 303 F.3d at 267 (internal citations and quotations omitted); see also *Heller v. Shaw Indus.,Inc*, 167 F.3d 146,155 (3d Cir. 1999) ("the reliability analysis applies to all aspects of an expert's testimony: the methodology, the facts underlying the expert's opinion, the link between the facts and the conclusion, et alia.")

Here the Government, as the proponent of the challenged testimony, bears the initial burden of proving its reliability and relevance by a preponderance of proof. *Liberty Media corp. v. Vivendi Universal*, 874 F.Supp.169,172 (S.D.N.Y. 2012).

Applying the *Daubert* Standard, The OCME's FST Software does

Not Produce Results that are generally Accepted as Reliable within the Scientific Community

The OCME's FST software has not crossed from experimental science to demonstrably accurate science that has been generally accepted as reliable within the forensic DNA community. Several facts amply demonstrate that the FST technique has not been generally accepted as reliable.

<u>The OCME is Alone in Using FST</u>

First, the OCME is the *only* laboratory in the United States that uses the FST software for purposes of analyzing DNA evidence to use in court against a criminal defendant. Alone, this fact shows that the technique is novel. If the technique had been recognized as reliable and is

generally accepted, it would be more widely used in the United States than in just one laboratory. Indeed, if reliability and general acceptance existed, then it may be borderline negligent for other forensic laboratories in the United States not to have investigated using FST themselves, let alone to have adopted it for use in criminal cases.

There has been Insufficient Peer Review of FST

Second, the opinions of other experts in the forensic DNA scientific community, or the lack thereof, weigh against this Court permitting the prosecution to offer expert testimony relating to the FST technique. There is a paucity of any peer review of the OCME's methodology in creating FST, the validation studies conducted, or the reliability of the results produced by FST.

Estimated drop-out rates, which form the backbone of the FST software, were empirically determined by the OCME according to quantitation values of given DNA samples.[2] Exhibit D at 757. Other probabilistic software modules, however, estimate drop-our rates according to peak heights and peak height ratios, a method endorsed by the DNA Commission of the International Society of Forensic Genetics. *Id.* at 681. "The lower the peak height of a 'surviving' allele, the greater the probability that an unseen companion allele has dropped out." *Id.* The OCME's development of the FST software thus *rejected* the method advocated by the DNA Commission of the International Society of Forensic Genetics in its publication, and instead "elected to empirically estimate drop-out rates as a function of the total amount of template DNA in a sample." Exhibit D at 757. Indeed, as revealed at the *Frye* hearing conducted before Justice Dwyer, *no other laboratory in the world expresses drop-out rate as a function of the total*

[2] This is discussed at length in the *Frye* hearing presided over in Brooklyn by Justice Dwyer in *People v. Collins & Peaks*, the transcript of which can be made available upon request.

quantity of DNA, and yet this is precisely what the OCME has done in developing the formulas upon which its FST software relies for accuracy.

Publications concerning the advent of probabilistic methods like FST opine about the validity of such methods, and offer recommendations to laboratories considering such methods, as new and novel procedures that are far from mainstream, especially in the United States. Rather than reflecting peer review and confirming general acceptance, peer-reviewed articles on the subject demonstrate the beginning of the process by which general acceptance of FST, *might perhaps someday* be obtained.

FST Assumes the Accuracy of Mixture Interpretation, Rendering an Unreliable Result

The assumption that allelic drop-out occurs is built into the OCME's FST software and forms the basis for its statistical calculations. *E.g.* Exhibit D. There are many controversial assumptions that must be invoked before FST calculates a likelihood ratio, and the resultant likelihood ratio is only as good as the assumptions used to calculate it. In other words, if the calculation is based on an erroneous assumption (for example, that the mixture contains the profiles of two, not three, people, or vice-versa, or if the drop-out rate, determined by quantity of template DNA rather than peak height ratio is wrong), the calculation is of limited, if any probative value whatsoever.

In 2009, the National Academy of Science issued a groundbreaking Report that reviewed forensic science disciplines offered in court and distinguished DNA evidence from other "forensic" disciplines, such as fingerprint and tool mark identification. It differentiated these disciplines, noting the reliable and non-subjective nature of DNA analysis. *See generally Strengthening Forensic Science in the United States: A Path Forward*, National Academy of Science, at 130 (2009).

Yet mixture analysis, drop-out rate estimation, and other interpretation of the data upon which the FST program relies is based on the OCME's protocols and the assigned criminalist's own subjective interpretation of the data in a given case. After the assigned analyst reviews the electropherograms and makes a subjective determination regarding which alleles are present at each locus in a mixture sample, he or she types this information, along with any known comparison profiles, into the FST software. The analyst also sets the parameters—likewise subjectively determine—necessary to run the program including, for example, whether the calculation should be based on a two- or three-person mixture, as subjectively determined by the analyst after reviewing the electronic data. The software then outputs a "Forensic Statistic Comparison Report." In this regard, FST is subjective and falls well beyond the types of DNA analysis endorsed by the NAS Report.

WHEREFORE, this Court should preclude the Government from introducing any evidence about FST or the result it produced in this case or, in the alternative, order a *Daubert* hearing, and grant any other relief as this Court deems just and proper.

Respectfully submitted,

_____/s/_____
Donald duBoulay,
Counsel for Dean Jones
305 Broadway, Suite 602
New York, NY 10007

New York, New York
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